BIOCHEMISTRY

COMAPARISON OF THE ELECTRON TRANSFER PROPERTIES OF WILD TYPE GLUTARYL COENZYME A WITH MUTATED FORMS OF THE ENZYME

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Glutaryl Coenzyme A Dehydrogenase (GCD) is an FAD containing mitochondrial enzyme involved in the degradative pathway of the amino acids lysine, hydroxylysine and tryptophan. Specifically, this enzyme catalyzes the conversion of glutaryl coenzyme A to the shorter chain crotonyl coenzyme A in an oxidative decarboxylation reaction. This study sought to compare the electron transfer properties of the wild type enzyme with the arginine at position 94 replaced with glutamine (R94Q) and glutamate at position 370 replaced with glutamine (E370Q) mutated forms of the enzyme using electrochemical techniques. Both of these mutations are located within the active site of the enzyme and are disease causing mutations. The glutamine at position 370 is the proton acceptor in the catalytic process and the arginine at 94 is believed to be involved in the binding of the substrate and may also be involved in other aspects of enzymatic activity. These mutations were found to alter the midpoint potential of the enzyme. Contrary to wild type GCD, both mutated forms may also demonstrate red radical formation upon reduction in the uncomplexed state.